

SEQUENCE LISTING

<110> Kapeller-Libermann, Rosana
White, David
MacBeth, Kyle J.

<120> 2786, A NOVEL HUMAN AMINOPEPTIDASE

<130> 5800-62

<140> US 09/443,795

<141> 1999-11-19

<160> 7

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 650

<212> PRT

<213> Homo sapiens

<400> 1

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Ala	Phe	Glu	Leu	Leu	His	Leu	His	Leu	Asp	Leu	Arg	Ala	Glu	Phe	Gly
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Pro	Pro	Gly	Pro	Gly	Ala	Gly	Ser	Arg	Gly	Leu	Ser	Gly	Thr	Ala	Val
			50			55					60				
Leu	Asp	Leu	Arg	Cys	Leu	Glu	Pro	Glu	Gly	Ala	Ala	Glu	Leu	Arg	Leu
65				70					75					80	
Asp	Ser	His	Pro	Cys	Leu	Glu	Val	Thr	Ala	Ala	Ala	Leu	Arg	Arg	Glu
				85					90					95	
Arg	Pro	Gly	Ser	Glu	Glu	Pro	Pro	Ala	Glu	Pro	Val	Ser	Phe	Tyr	Thr
			100					105					110		
Gln	Pro	Phe	Ser	His	Tyr	Gly	Gln	Ala	Leu	Cys	Val	Ser	Phe	Pro	Gln
			115				120					125			
Pro	Cys	Arg	Ala	Ala	Glu	Arg	Leu	Gln	Val	Leu	Leu	Thr	Tyr	Arg	Val
			130			135					140				
Gly	Glu	Gly	Pro	Gly	Val	Cys	Trp	Leu	Ala	Pro	Glu	Gln	Thr	Ala	Gly
145				150					155					160	
Lys	Lys	Lys	Pro	Phe	Val	Tyr	Thr	Gln	Gly	Gln	Ala	Val	Leu	Asn	Arg
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Ala	Phe	Phe	Pro	Cys	Phe	Asp	Thr	Pro	Ala	Val	Lys	Tyr	Lys	Tyr	Ser
			180					185					190		
Ala	Leu	Ile	Glu	Val	Pro	Asp	Gly	Phe	Thr	Ala	Val	Met	Ser	Ala	Ser
			195				200					205			
Thr	Trp	Glu	Lys	Arg	Gly	Pro	Asn	Lys	Phe	Phe	Phe	Gln	Met	Cys	Gln
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Pro	Ile	Pro	Ser	Tyr	Leu	Ile	Ala	Leu	Ala	Ile	Gly	Asp	Leu	Val	Ser
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 <222> (62)...(2011)

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 Met Ala Ser Gly Glu His Ser Pro Gly Ser Gly Ala Ala Arg Arg Pro
 1 5 10 15
 ctg cac tcc gcg cag gct gtg gac gtg gcc tcg gcc tcc aac ttc cgg 157
 Leu His Ser Ala Gln Ala Val Asp Val Ala Ser Ala Ser Asn Phe Arg
 20 25 30
 gcc ttt gag ctg ctg cac ttg cac ctg gac ctg cgg gct gag ttc ggg 205
 Ala Phe Glu Leu Leu His Leu His Leu Asp Leu Arg Ala Glu Phe Gly
 35 40 45
 cct cca ggg ccc ggc gca ggg agc cgg ggg ctg agc ggc acc gcg gtc 253
 Pro Pro Gly Pro Gly Ala Gly Ser Arg Gly Leu Ser Gly Thr Ala Val
 50 55 60
 ctg gac ctg cgc tgc ctg gag ccc gag ggc gcc gcc gag ctg cgg ctg 301
 Leu Asp Leu Arg Cys Leu Glu Pro Glu Gly Ala Ala Glu Leu Arg Leu
 65 70 75 80
 gac tcg cac ccg tgc ctg gag gtg acg gcg gcg gcg ctg cgg cgg gag 349
 Asp Ser His Pro Cys Leu Glu Val Thr Ala Ala Ala Leu Arg Arg Glu
 85 90 95
 cgg ccc ggc tcg gag gag ccg cct gcg gag ccc gtg agc ttc tac acg 397
 Arg Pro Gly Ser Glu Glu Pro Pro Ala Glu Pro Val Ser Phe Tyr Thr
 100 105 110
 cag ccc ttc tcg cac tat ggc cag gcc ctg tgc gtg tcc ttc ccg cag 445
 Gln Pro Phe Ser His Tyr Gly Gln Ala Leu Cys Val Ser Phe Pro Gln
 115 120 125
 ccc tgc cgc gcc gcc gag cgc ctc cag gtg ctg ctc acc tac cgc gtc 493
 Pro Cys Arg Ala Ala Glu Arg Leu Gln Val Leu Leu Thr Tyr Arg Val
 130 135 140
 ggg gag gga ccc ggg gtt tgc tgg ttg gct ccc gag cag aca gca gga 541
 Gly Glu Gly Pro Gly Val Cys Trp Leu Ala Pro Glu Gln Thr Ala Gly
 145 150 155 160
 aag aag aag ccc ttc gtg tac acc cag ggc cag gct gtc cta aac cgg 589
 Lys Lys Lys Pro Phe Val Tyr Thr Gln Gly Gln Ala Val Leu Asn Arg
 165 170 175
 gcc ttc ttc cct tgc ttc gac acg cct gct gtt aaa tac aag tat tca 637
 Ala Phe Phe Pro Cys Phe Asp Thr Pro Ala Val Lys Tyr Lys Tyr Ser
 180 185 190

gct ctt att gag gtc cca gat ggc ttc aca gct gtg atg agt gct agc Ala Leu Ile Glu Val Pro Asp Gly Phe Thr Ala Val Met Ser Ala Ser																	685
195																	
200																	
205																	
acc tgg gag aag aga ggt cca aat aag ttc ttc ttc cag atg tgt cag																	733
Thr Trp Glu Lys Arg Gly Pro Asn Lys Phe Phe Phe Gln Met Cys Gln																	
210																	
215																	
220																	
ccc atc ccc tcc tat ctg ata gct ttg gcc atc gga gat ctg gtt tcg																	781
Pro Ile Pro Ser Tyr Leu Ile Ala Leu Ala Ile Gly Asp Leu Val Ser																	
225																	
230																	
235																	
240																	
gct gaa gtt gga ccc agg agc cgg gtg tgg gct gag ccc tgc ctg att																	829
Ala Glu Val Gly Pro Arg Ser Arg Val Trp Ala Glu Pro Cys Leu Ile																	
245																	
250																	
255																	
gat gct gcc aat gag gag tac aac ggg gtg ata gaa gaa ttt ttg gca																	877
Asp Ala Ala Asn Glu Glu Tyr Asn Gly Val Ile Glu Glu Phe Leu Ala																	
260																	
265																	
270																	
aca gga gag aag ctt ttt gga cct tat gtt tgg gga agg tat gac ttg																	925
Thr Gly Glu Lys Leu Phe Gly Pro Tyr Val Trp Gly Arg Tyr Asp Leu																	
275																	
280																	
285																	
ctc ttc atg cca ccg tcc ttt cca ttt gga gga atg gag aac cct tgt																	973
Leu Phe Met Pro Pro Ser Phe Pro Phe Gly Gly Met Glu Asn Pro Cys																	
290																	
295																	
300																	
ctg acc ttt gtc acc ccc tgc ctg cta gct ggg gac cgc tcc ttg gca																	1021
Leu Thr Phe Val Thr Pro Cys Leu Leu Ala Gly Asp Arg Ser Leu Ala																	
305																	
310																	
315																	
320																	
gat gtc atc atc cat gag atc tcc cac agt tgg ttt ggg aac ctg gtc																	1069
Asp Val Ile Ile His Glu Ile Ser His Ser Trp Phe Gly Asn Leu Val																	
325																	
330																	
335																	
acc aac gcc aac tgg ggt gaa ttc tgg ctc aat gaa ggt ttc acc atg																	1117
Thr Asn Ala Asn Trp Gly Glu Phe Trp Leu Asn Glu Gly Phe Thr Met																	
340																	
345																	
350																	
tac gcc cag agg agg atc tcc acc atc ctc ttt ggc gct gcg tac acc																	1165
Tyr Ala Gln Arg Arg Ile Ser Thr Ile Leu Phe Gly Ala Ala Tyr Thr																	
355																	
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tgc ttg gag gct gca acg ggg cgg gct ctg ctg cgt caa cac atg gac																	1213
Cys Leu Glu Ala Ala Thr Gly Arg Ala Leu Leu Arg Gln His Met Asp																	
370																	
375																	
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atc act gga gag gaa aac cca ctc aac aag ctc cgc gtg aag att gaa																	1261
Ile Thr Gly Glu Glu Asn Pro Leu Asn Lys Leu Arg Val Lys Ile Glu																	
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395																	
400																	
cca ggc gtt gac ccg gac gac acc tat aat gag acc ccc tac gag aaa																	1309
Pro Gly Val Asp Pro Asp Asp Thr Tyr Asn Glu Thr Pro Tyr Glu Lys																	
405																	
410																	
415																	

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Gly Phe Cys Phe Val Ser Tyr Leu Ala His Leu Val Gly Asp Gln Asp	
420 425 430	
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Gln Phe Asp Ser Phe Leu Lys Ala Tyr Val His Glu Phe Lys Phe Arg	
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agc atc tta gcc gat gac ttt ctg gac ttc tac ttg gaa tat ttc cct	1453
Ser Ile Leu Ala Asp Asp Phe Leu Asp Phe Tyr Leu Glu Tyr Phe Pro	
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Glu Leu Lys Lys Lys Arg Val Asp Ile Ile Pro Gly Phe Glu Phe Asp	
465 470 475 480	
cga tgg ctg aat acc ccc ggc tgg ccc ccg tac ctc cct gat ctc tcc	1549
Arg Trp Leu Asn Thr Pro Gly Trp Pro Pro Tyr Leu Pro Asp Leu Ser	
485 490 495	
cct ggg gac tca ctc atg aag cct gct gaa gag cta gcc caa ctg tgg	1597
Pro Gly Asp Ser Leu Met Lys Pro Ala Glu Glu Leu Ala Gln Leu Trp	
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Ala Ala Glu Glu Leu Asp Met Lys Ala Ile Glu Ala Val Ala Ile Ser	
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aaa tcc cct ctc cct cct ggg aat gtg aaa aaa ctt gga gac aca tac	1741
Lys Ser Pro Leu Pro Pro Gly Asn Val Lys Lys Leu Gly Asp Thr Tyr	
545 550 555 560	
cca agt atc tca aat gcc cgg aat gca gag ctc cgg ctg cga tgg ggc	1789
Pro Ser Ile Ser Asn Ala Arg Asn Ala Glu Leu Arg Leu Arg Trp Gly	
565 570 575	
caa atc gtc ctt aag aac gac cac cag gaa gat ttc tgg aaa gtg aag	1837
Gln Ile Val Leu Lys Asn Asp His Gln Glu Asp Phe Trp Lys Val Lys	
580 585 590	
gag ttc ctg cat aac cag ggg aag cag aag tat aca ctt ccg ctg tac	1885
Glu Phe Leu His Asn Gln Gly Lys Gln Lys Tyr Thr Leu Pro Leu Tyr	
595 600 605	
cac gca atg atg ggt ggc agt gag gtg gcc cag acc ctc gcc aag gag	1933
His Ala Met Met Gly Gly Ser Glu Val Ala Gln Thr Leu Ala Lys Glu	
610 615 620	
act ttt gca tcc acc gcc tcc cag ctc cac agc aat gtt gtc aac tat	1981
Thr Phe Ala Ser Thr Ala Ser Gln Leu His Ser Asn Val Val Asn Tyr	
625 630 635 640	
gtc cag cag atc gtg gca ccc aag ggc agt tagaggctcg tgtgcatggc	2031

Val Gln Gln Ile Val Ala Pro Lys Gly Ser
645 650

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<223> Ribonucleoprotein Binding Site

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Gly Ser Cys Ile Phe Tyr Leu Ile Val Ala Xaa Phe Tyr Met
20 25 30

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<212> PRT
<213> Artificial Sequence

<220>
<223> Nuclear Localization Motif

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<210> 5
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<223> potential catalytic site

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<223> potential catalytic site

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